

Supplementary Table S1

cluster transition	sites involved	patches involved
HK68-EN72	122,144,155,188,207	1,2,5
EN72-VI75	137,145,164,189,193, 53,278,174,102,213,217,230	1,2,3,6
VI75-TX77	137,158,164,193,50, 53,174,201, 213, 230, 82, 260	1,2,3,6
TX77-BA79	133,143,146,156,160, 197,53,54,172, 217, 244,162,82	1
BA79-SI87	124,155,189	1
SI87-BE89	145	2
BE89-BE92	133,145,156,190,262	1,2
BE92-WU95	145	2
WU95-SY97	62,156,158,196,276	1,3,4
SY97-FU02	131,155,156,50,75, 83,25,202,222,225	1,3,4

Table S 1: Changes between consensus sequences representing consecutive pre-dominating and antigenic variants of human influenza A/H3N2 viruses according to Smith *et al.* [51], and patches involved according to Table [1].